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EXAMINER	
COLLINS, CYNTHIA E	

ART UNIT	PAPER NUMBER
1638	

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/031,818	OZEKI ET AL.	
	Examiner	Art Unit	
	Cynthia Collins	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *19 April 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,3-5,8,11,12 and 21-28* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,3-5,8,11,12 and 21* is/are rejected.

7)☒ Claim(s) *22-28* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *17 January 2002* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *04/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Applicant's election without traverse of Group I, claims 1, 3-5, 8, 10-12 and 21-28, in the reply filed on April 19, 2004, is acknowledged.

Claims 2, 6-7, 9-10 and 13-20 are cancelled.

Claims 8, 21 and 22 are currently amended.

Claims 1, 3-5, 8, 11-12 and 21-28 are pending.

Information Disclosure Statement

An initialed and dated copy of Applicant's IDS form 1449, filed April 19, 2002 is attached to the instant Office action.

Claim Objections

Claims 22 and 25, and claims 23-24 and 26-28 dependent thereon, are objected to under 37 CFR 1.75(c) as being in improper form because a multiple dependent claim cannot depend from any other multiple dependent claim. See MPEP § 608.01(n). Accordingly, claims 22 and 25, and claims 23-24 and 26-28 dependent thereon, have not been further treated on the merits.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1, 3-5, 8 and 11 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 1 is drawn to a miniature inverted-repeat transposable element (MITE)-like element capable of causing duplication of the target sequence: (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene, which has perfect or imperfect terminal inverted repeat sequences in the 5' and 3' terminal regions. Claim 3 is drawn to a MITE-like element as claimed in Claim 1 which contains, in the sequence thereof, a plurality of repetitions of at least one of the nucleotide sequences represented by the formula (1): XttgcaaY (wherein X represents g or t and Y represents a or c) or the formula (2): Zatgcaa (wherein Z represents t or a). Claim 4 is drawn to a MITE-like element as claimed in Claim 1 which has, as terminal inverted repeat sequences, a nucleotide sequence shown under SEQ ID NO: 10 in the 5' terminal region and a nucleotide sequence shown under SEQ ID NO: 11 in the 3' terminal region. Claim 5 is drawn to a MITE-like element comprising the following DNA (a) or (b): (a) a DNA having a nucleotide sequence shown under SEQ ID NO: 1; (b) a DNA capable of hybridizing with a DNA having a complementary sequence to the above nucleotide sequence (a) under stringent conditions and capable of causing duplication of the target sequence: (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene. Claim 8 is drawn to a transcriptional activation element characterized by containing at least one MITE-like element according to any of claims 1, 3, 4 or 5 as a transposable element. Claim 11 is drawn to a

transcriptional activation element as claimed in Claim 8, wherein the transposable element is a tandem coupling product from a MITE-like element comprising the following DNA (a) or (b): (a) a DNA having the nucleotide sequence shown under SEQ ID NO: 1; (b) a DNA capable of hybridizing with a DNA having a complementary sequence to the above nucleotide sequence (a) under stringent conditions and capable of causing duplication of (A)nG(A)n [n being an integer of not less than l] at the site of insertion thereof in a genomic gene, and a MITE-like element comprising the following DNA (c) or (d): (c) a DNA having the nucleotide sequence shown under SEQ ID NO:2; (d) a DNA capable of hybridizing with a DNA having a complementary sequence to the above nucleotide sequence (c) under stringent conditions and capable of causing duplication of TA at the site of insertion thereof in a genomic gene.

With respect to MITE-like elements, the specification describes the promoter region of a carrot (*Daucus carota* L. cv. Kurodagosun) phenylalanine ammonia-lyase (PAL) gene, gDCPAL3, as containing two different miniature inverted-repeat transposable elements (MITEs) having imperfect inverted repeat sequences and being located at two distinct sites, a 299 bp MITE of SEQ ID NO:2 (named IS1) located at positions -1897 to -1599 of the gDCPAL3 promoter, and a 769 bp MITE of SEQ ID NO:1 (named IS2) located at positions -1157 to -389 of the gDCPAL3 promoter (page 39; pages 43-44). The elected IS2 MITE of SEQ ID NO:1 is further described as having 158 bp imperfect inverted terminal repeat sequences, with the nucleotide sequence of SEQ ID NO:10 being located in the 5' terminal region and the nucleotide sequence of SEQ ID NO: 11 being located in the 3' terminal region (page 22; page 45). The elected IS2 MITE of SEQ ID NO:1 is also further described as being associated with a target duplication sequence of AAAAGAAAA at the site of its insertion into its gDCPAL3 target gene

(page 45). The IS2 MITE of SEQ ID NO:1 is additionally described as having no homology with known transposable elements, such that it constitutes a novel family belonging to none of the so far known transposable element families (page 45).

The specification does not describe MITE-like elements that are capable of causing duplication of a genus of target sequences (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene. Instead the specification describes a single MITE-like element of SEQ ID NO:1 associated with the single target duplication sequence AAAAGAAAA. The specification also does not describe a genus of MITE-like elements that are capable of causing duplication of a genus of target sequences (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene and that have a genus of perfect terminal inverted repeat sequences in their 5' and 3' terminal regions, or that have a genus of imperfect terminal inverted repeat sequences in their 5' and 3' terminal regions. Instead the specification describes a single MITE-like element of SEQ ID NO:1 having the nucleotide sequence shown under SEQ ID NO: 10 in the 5' terminal region and the nucleotide sequence shown under SEQ ID NO: 11 in the 3' terminal region. The specification additionally does not describe a genus of MITE-like elements that are capable of causing duplication of a genus of target sequences (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene and that contain a genus of a plurality of repetitions of at least one of the nucleotide sequences represented by the formula (1): XttgcaaY (wherein X represents g or t and Y represents a or c) or the formula (2): Zatgcaa (wherein Z represents t or a). Instead the specification describes a single MITE-like element having the nucleotide sequence of SEQ ID NO:1. The specification further does not describe a genus of MITE-like elements that are

capable of causing duplication of the target sequence: (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene and that comprise a genus of DNAs capable of hybridizing with a DNA having a complementary sequence to SEQ ID NO:1 under stringent conditions. Instead the specification describes the single MITE-like element having the nucleotide sequence of SEQ ID NO:1 itself.

With respect to genetic constructs, the specification describes three MITE/promoter fusion constructs wherein the IS2 MITE of SEQ ID NO:1 is cloned upstream of a CaMV 35S promoter: a first construct where IS2 is cloned upstream of the 35S promoter (IS2-35S/SK, page 48 and Figure 8), a second construct where IS2 and IS1 are cloned in tandem (SEQ ID NO:3, page 31) upstream of the 35S promoter (IS12-35S/SK2, pages 48-49 and Figure 9), and a third construct where IS2 and IS1 are cloned in their native configuration (SEQ ID NO:14, page 31) upstream of the 35S promoter (MU3-35S/SK, pages 49-50 and Figure 10). The specification further describes three plant gene expression vectors where the MITE/promoter fusion constructs are cloned between the nptII selectable marker gene and the GUS reporter gene of the plant gene expression vector pABNHm1 (pIS2-35S/AB35S, pIS12-35S/AB35S, and pMU3-35S/AB35S, pages 50-52 and Figure 11). The specification additionally describes tobacco, carrot and rice plant cells transformed with the three plant gene expression vectors as having increased transformation efficiency or improved regeneration efficiency, as compared to transformed control plant cells (pages 59-69).

The specification does not describe or characterize any element or construct containing at least one MITE-like element that has transcriptional activation activity. The specification also does not describe or characterize any transcriptional activation element containing at least one

MITE-like element that functions as a transposable element. The specification additionally does not describe a genus of recombinant DNA constructs comprising a tandem coupling product from a MITE-like element, but rather a single DNA construct of SEQ ID NO:3 in which IS2 (SEQ ID NO:1) and IS1 (SEQ ID NO:2) are cloned in tandem.

The Federal Circuit has recently clarified the application of the written description requirement. The court stated that "A description of a genus of cDNAs may be achieved by means of recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." See *University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1569; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). The court has also affirmed the PTO's applicable standard for determining compliance with the written description requirement, quoting from the PTO's Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112, P1, "Written Description" Requirement, 66 Fed. Reg. 1099, 1106, where it is set forth that the written description requirement can be met by "show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ... i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." See *Enzo Biochem Inc. v. Gen-Probe Inc.*, 63 USPQ2d 1609, 1613 (CAFC 2002)

In the instant case Applicant has not described a representative number of species falling within the scope of the genus that encompasses any MITE-like element obtained from any source that is capable of causing duplication of any target sequence of (A)nG(A)n [n being an integer of

not less than 1] at the site of insertion thereof in a genomic gene, or the genus that encompasses any MITE-like element obtained from any source as claimed in Claim 1 which contains, in the sequence thereof, a plurality of repetitions of at least one of the nucleotide sequences represented by the formula (1): XttgcaaY (wherein X represents g or t and Y represents a or c) or the formula (2): Zatgcaa (wherein Z represents t or a), or the genus that encompasses any MITE-like element obtained from any source as claimed in Claim 1 which has, as terminal inverted repeat sequences, a nucleotide sequence shown under SEQ ID NO: 10 in the 5' terminal region and a nucleotide sequence shown under SEQ ID NO: 11 in the 3' terminal region, or the genus that encompasses any MITE-like element obtained from any source comprising a DNA capable of hybridizing with a DNA having a complementary sequence to the nucleotide sequence of SEQ ID NO:1 under any stringency conditions and capable of causing duplication of the target sequence: (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene, nor the structural features unique to any genus above that are correlated with the function of causing duplication of the target sequence (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene. In the instant case Applicant also has not described a representative number of species falling within the scope of the genus that encompasses any transcriptional activation element characterized by containing at least one MITE-like element according to any of claims 1, 3, 4 or 5 as a transposable element, nor the structural features unique to the genus that are correlated with the function of transcriptional activation or transposition.

Claims 1, 3-5, 8, 11-12 and 21 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated miniature inverted-repeat transposable element (MITE)-like element having the nucleotide sequence of SEQ ID NO:1, a recombinant DNA element having the nucleotide sequence of SEQ ID NO:3, and a recombinant DNA element having the nucleotide sequence of SEQ ID NO:14, does not reasonably provide enablement for other isolated MITE-like elements, or isolated MITE-like elements that are capable of causing duplication of a target sequence, or other recombinant DNA elements, or recombinant DNA elements that activate transcription or that transpose. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Claim 1 is drawn to a miniature inverted-repeat transposable element (MITE)-like element capable of causing duplication of the target sequence: (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene, which has perfect or imperfect terminal inverted repeat sequences in the 5' and 3' terminal regions. Claim 3 is drawn to a MITE-like element as claimed in Claim 1 which contains, in the sequence thereof, a plurality of repetitions of at least one of the nucleotide sequences represented by the formula (1): XttgcaaY (wherein X represents g or t and Y represents a or c) or the formula (2): Zatgcaa (wherein Z represents t or a). Claim 4 is drawn to a MITE-like element as claimed in Claim 1 which has, as terminal inverted repeat sequences, a nucleotide sequence shown under SEQ ID NO: 10 in the 5' terminal region and a nucleotide sequence shown under SEQ ID NO: 11 in the 3' terminal region. Claim 5 is drawn to a MITE-like element comprising the following DNA (a) or (b): (a) a DNA having a nucleotide sequence shown under SEQ ID NO: 1; (b) a DNA capable of hybridizing

with a DNA having a complementary sequence to the above nucleotide sequence (a) under stringent conditions and capable of causing duplication of the target sequence: (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene. Claim 8 is drawn to a transcriptional activation element characterized by containing at least one MITE-like element according to any of claims 1, 3, 4 or 5 as a transposable element. Claim 11 is drawn to a transcriptional activation element as claimed in Claim 8, wherein the transposable element is a tandem coupling product from a MITE-like element comprising the following DNA (a) or (b): (a) a DNA having the nucleotide sequence shown under SEQ ID NO: 1; (b) a DNA capable of hybridizing with a DNA having a complementary sequence to the above nucleotide sequence (a) under stringent conditions and capable of causing duplication of (A)nG(A)n [n being an integer of not less than l] at the site of insertion thereof in a genomic gene, and a MITE-like element comprising the following DNA (c) or (d): (c) a DNA having the nucleotide sequence shown under SEQ ID NO:2; (d) a DNA capable of hybridizing with a DNA having a complementary sequence to the above nucleotide sequence (c) under stringent conditions and capable of causing duplication of TA at the site of insertion thereof in a genomic gene. Claim 12 is drawn to a transcriptional activation element comprising a DNA having the nucleotide sequence shown under SEQ ID NO:3. Claim 21 is drawn to transcriptional activation element comprising a DNA having the nucleotide sequence shown as SEQ ID NO: 14.

With respect to making MITE-like elements, the specification discloses the cloning of a carrot (*Daucus carota* L. cv. Kurodagosun) phenylalanine ammonia-lyase (PAL) gene, gDCPAL3 (page 39). The specification also discloses that the promoter region of gDCPAL3 contains two different miniature inverted-repeat transposable elements (MITEs) that have

imperfect inverted repeat sequences and that are located at two distinct sites in the gDCPAL3 promoter, a 299 bp MITE of SEQ ID NO:2 (named IS1) located at positions -1897 to -1599 of the gDCPAL3 promoter, and a 769 bp MITE of SEQ ID NO:1 (named IS2) located at positions -1157 to -389 of the gDCPAL3 promoter (page 39; pages 43-44). The IS2 MITE of SEQ ID NO:1 which corresponds to the elected invention is further disclosed as having 158 bp imperfect inverted terminal repeat sequences, with the nucleotide sequence of SEQ ID NO:10 being located in the 5' terminal region and the nucleotide sequence of SEQ ID NO: 11 being located in the 3' terminal region (page 22; page 45). The IS2 MITE of SEQ ID NO:1 is also disclosed as being associated with a target duplication sequence of AAAAGAAAA at the site of its insertion into its target gene (page 45). The IS2 MITE of SEQ ID NO:1 is additionally disclosed as having no homology with known transposable elements, such that it constitutes a novel family belonging to none of the so far known transposable element families (page 45).

The specification does not disclose any MITE-like elements that are capable of causing duplication of a genus of target sequences (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene. The specification also does not disclose MITE-like elements that have a genus of perfect terminal inverted repeat sequences in their 5' and 3' terminal regions, or that have a genus of imperfect terminal inverted repeat sequences in their 5' and 3' terminal regions. The specification additionally does not disclose MITE-like elements that contain a genus of a plurality of repetitions of at least one of the nucleotide sequences represented by the formula (1): XttgcaaY (wherein X represents g or t and Y represents a or c) or the formula (2): Zatgcaa (wherein Z represents t or a). The specification further does not disclose

MITE-like elements that comprise DNA capable of hybridizing with a DNA having a complementary sequence to SEQ ID NO:1 under any stringency conditions.

With respect to making genetic constructs, the specification discloses the construction of three MITE/promoter fusion constructs wherein the IS2 MITE of SEQ ID NO:1 is cloned upstream of a CaMV 35S promoter: a first construct where IS2 is cloned upstream of the 35S promoter (IS2-35S/SK, page 48 and Figure 8), a second construct where IS2 and IS1 are cloned in tandem (SEQ ID NO:3, page 31) upstream of the 35S promoter (IS12-35S/SK2, pages 48-49 and Figure 9), and a third construct where IS2 and IS1 are cloned in their native configuration (SEQ ID NO:14, page 31) upstream of the 35S promoter (MU3-35S/SK, pages 49-50 and Figure 10). The specification further discloses the construction of three different plant gene expression vectors where the MITE/promoter fusion constructs comprising the elected IS2MITE of SEQ ID NO:1 are cloned between the nptII selectable marker gene and the GUS reporter gene of the plant gene expression vector pABNHm1 (pIS2-35S/AB35S, pIS12-35S/AB35S, and pMU3-35S/AB35S, pages 50-52 and Figure 11).

The specification does not disclose how to make or use any MITE-like element or genetic construct that has transcriptional activation activity. The specification also does not disclose how to make or use any transcriptional activation element containing at least one MITE-like element that functions as a transposable element. The specification additionally does not disclose how to make or use any other recombinant DNA constructs comprising other tandem coupling products of MITE-like elements.

With respect to using the disclosed MITE-like elements and genetic constructs, the specification teaches the use of plasmids pIS2-35S/AB35S, pIS12-35S/AB35S, and pMU3-

35S/AB35S to transform tobacco, carrot and rice plant cells by *Agrobacterium*-mediated transformation. An increased yield of transformant calli was observed when cultured BY-2 tobacco cells were transformed with pIS2-35S/AB35S or pIS12-35S/AB35S, the yield being 1.6 to 2.6 X higher as compared to transformed control cells selected on 100ug/ml kanamycin, and 10 X higher as compared to transformed control cells selected on 300ug/ml kanamycin, implying increased nptII gene expression as a consequence of the presence of the MITE/promoter fusions (pages 57 Table 1; page-58). Increased GUS activity was also observed when cultured BY-2 tobacco cells were transformed with pIS12-35S/AB35S, the activity being 2.6 X higher as compared to transformed control cells (Figure 13; pages 59-60). An increase in shoot regeneration efficiency was observed when SR1 tobacco leaf discs were transformed with pIS2-35S/AB35S or pIS12-35S/AB35S, the efficiency being 1.4 to 2 X higher as compared to transformed control leaf discs, implying increased nptII gene expression as a consequence of the presence of the MITE/promoter fusions (page 62 Table 2; pages 62-63). Improved regeneration efficiency in the presence or absence of 2,4-D was observed when carrot somatic embryos were transformed with pIS2-35S/AB35S, pIS12-35S/AB35S, and pMU3-35S/AB35S as compared to transformed control somatic embryos (page 65 Table 3; pages 63-66). Improved regeneration efficiency was observed when rice seeds were transformed with pIS2-35S/AB35S, the efficiency being 2 X higher as compared to transformed control leaf discs, implying increased nptII gene expression as a consequence of the presence of the MITE/promoter fusions as compared to transformed control somatic embryos (page 69 Table 4; pages 66-69).

The full scope of the claimed invention is not enabled because the specification does not provide sufficient guidance with respect to where and how to obtain other MITE-like elements

that structurally and functionally resemble the IS2 MITE of SEQ ID NO:1. Such guidance is necessary because one cannot predictably obtain MITE-like elements that structurally and functionally resemble the IS2 MITE of SEQ ID NO:1 from other sources. The specification itself discloses at page 45 that the IS2 MITE of SEQ ID NO:1 has no homology with known transposable elements, such that it constitutes a novel family belonging to none of the so far known transposable element families. Furthermore, the prior art also teaches that other plant MITE-like elements may be detected in some plant species but not others. See, for example, Bureau et al., who teach that nine putative mobile element families, including the MITE-like elements Tourist and Stowaway, are detected in the genome of rice, but not *Arabidopsis* (Proc. Natl. Acad. Sci. USA, August 1996, Vol. 93, pages 8524-8529, Applicant's IDS, see page 8524 abstract and page 8527 column 1 last paragraph). Given the unpredictability of identifying other MITE-like elements that structurally and functionally resemble the IS2 MITE of SEQ ID NO:1 in other plant species, it would require undue experimentation for one skilled in the art to identify and clone from undisclosed sources such elements, as one skilled in the art would have to first identify by trial and error those plant species that potentially harbor such elements, and then isolate and characterize candidate element to confirm its identity.

The full scope of the claimed invention is also not enabled because the specification does not provide sufficient guidance with respect to how to use the disclosed MITE-like sequences to duplicate a target sequence or transpose. Such guidance is necessary because it is unpredictable whether the disclosed MITE-like sequences and genetic constructs would cause duplication of a target sequence or transpose, since neither Applicant nor the prior art have established that any MITE has these functional attributes. See, for example, Wessler et al. who teach that while

MITES have structural elements in common with known transposable elements, MITES have no coding potential, and it is not known by what mechanism (DNA or RNA) a MITE may transpose (Current Opinion in Genetics and Development, 1995, Vol. 5, pages 814-821, Applicant's IDS, see page 818 column 1 third paragraph and column 2 last paragraph). Wessler et al. further teach that if MITES are DNA elements their mobilization would require transposase activity encoded by another element or genetic locus, and that no MITE has been shown to excise, which may indicate low transposase activity or that MITES present in the genome are no longer transpositionally active (page 819 column 1 first paragraph). Given the uncertainty of whether and how MITE-like sequences could cause duplication of a target sequence or transpose, it would require undue experimentation for one skilled in the art to determine how to induce a MITE to exhibit such activity, as one skilled in the art would have to identify by trial and error both a MITE transposition event and the other element or genetic locus that was the cause of the event.

The full scope of the claimed invention is additionally not enabled because the specification does not provide sufficient guidance with respect to how to use the disclosed MITE-like sequences to activate transcription. Such guidance is necessary because it is unpredictable whether the disclosed MITE-like sequences and recombinant DNA elements comprising these sequences actually function to activate transcription, since a variety of other different mechanisms other than transcriptional activation could be proposed to account for the increased transformation efficiency and improved regeneration efficiency observed in plant cells transformed with expression vectors comprising the disclosed MITE-like sequences and genetic constructs. For example, improved transgene integration could be proposed to account for the

observed increased transformation efficiency and improved regeneration efficiency. See Kumar et al., who teach that transgene silencing is known to be correlated with the insertion upon transformation of multiple transgene copies at the same chromosomal site and with the associated methylation of their promoters (Biotechniques, 2000, Vol. 28, No. 6, pages 1128-1137, see page 1128 abstract and first paragraph). A reduction in the number of multiple transgene copy insertions could also reasonably be proposed to account for the observed increased transformation efficiency and improved regeneration efficiency. Given the uncertainty of whether the disclosed MITE-like sequences actually function to activate transcription, it would require undue experimentation for one skilled in the art to determine how to induce a MITE to exhibit such activity, as one skilled in the art would have to evaluate whether a MITE inherently exhibits such activity, and would possibly have to further modify a MITE to exhibit such activity if it is not inherent.

Given the claim breadth, unpredictability and lack of guidance as discussed above, it would require undue experimentation for one skilled in the art to make and use the full scope of the claimed invention.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1, 3-5, 8, 11-12 and 21 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

Claims 1 and 3-5 are directed to a MITE-like element. Claims 8, 11-12 and 21 are directed to a transcriptional activation element. Claims 1, 3-5, 8, 11-12 and 21 as written do not sufficiently distinguish over nucleic acids as they exist naturally, because the claims do not particularly point out any non-naturally occurring products. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. See Diamond v. Chakrabarty, 447 U.S. 303, 206 USPQ 193 (1980). The claims should be amended to indicate the hand of the inventor, e.g., by insertion of "Isolated" or "Purified" or "Recombinant". See MPEP 2105.

Remarks

Claims 1, 3-5, 8, 11-12 and 21 are deemed free of the prior art, due to the failure of the prior art to teach or suggest a MITE-like element capable of causing duplication of the target sequence: (A)nG(A)n [n being an integer of not less than 1] at the site of insertion thereof in a genomic gene, which MITE-like element has perfect or imperfect terminal inverted repeat sequences in the 5' and 3' terminal region, which MITE-like element contains, in the sequence thereof, a plurality of repetitions of at least one of the nucleotide sequences represented by the formula (1): XttgcaaY (wherein X represents g or t and Y represents a or c) or the formula (2): Zatgcaa (wherein Z represents t or a), which MITE-like element has, as terminal inverted repeat sequences, a nucleotide sequence shown under SEQ ID NO: 10 in the 5' terminal region and a nucleotide sequence shown under SEQ ID NO: 11 in the 3' terminal region, and which MITE-like element comprises a DNA having a nucleotide sequence shown under SEQ ID NO: 1.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Cynthia Collins whose telephone number is (571) 272-0794. The examiner can normally be reached on Monday-Friday 8:45 AM -5:15 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on (571) 272-0804. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

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Cynthia Collins  7/9/04